Amendments to the Specification:

Please replace the title of the specification on page 1, line 1 with the following amended title:

TRANSGENIC PLANTS TRANSFORMED WITH A TRANSCRIPTIONAL REGULATOR[[S]] OF ABIOTIC STRESS

Please replace the first paragraph of the specification on page 1, lines 4-21, with the following amended paragraph:

This application ~~claims priority from copending~~ is a continuation-in-part of prior U.S. Patent Application No. 09/810,836, filed March 16, 2001 (now issued as U.S. Patent No. 6,835,540); and, this application is a continuation in part of prior U.S. Patent Application No. 10/412,699, filed April 10, 2003 (pending), which ~~claims priority from~~ is a continuation-in-part of prior U.S. Patent Application No. 09/394,519, filed September 13, 1999 (now abandoned) which claims benefit of U.S. Provisional Application No. 60/101,349, filed September 22, 1998, and U.S. Provisional Application No. 60/108,734, filed November 17, 1998; and, U.S. Patent Application No. 10/412,699 is also a continuation-in-part of prior U.S. Patent Application 09/533,392, filed March 22, 2000 (now abandoned), which claims benefit of U.S. Provisional Patent Application 60/125,814, filed March 23, 1999;~~ 10/171,468, filed June 14, 2002, U.S. Non-provisional Application No. 09/532,591, filed March 22, 2000, U.S. Non-provisional Application No. 09/533,029, filed March 22, 2000, U.S. Non-provisional Application No. 09/533,392, filed March 22, 2000, which in turned claimed priority from U.S. Provisional Patent Application 60/125,814, filed March 23, 1999;~~ and, this application is a continuation-in-part of prior U.S. Non-provisional Application No. 09/713,994, filed November 16, 2000 (pending), which ~~in turn claimed priority from~~ claims benefit of U.S. Provisional Patent Application No. 60/166,228, filed November 17, 1999 and U.S. Provisional Patent Application No. 60/227,439, filed August 22, 2000; ~~U.S. Non-provisional Application No. 09/394,519, filed September 13, 1999, which in turn claimed priority from U.S. Provisional Application No. 60/101,349, filed September 22, 1998, and U.S. Provisional Application No. 60/108,734, filed November 17, 1998; U.S. Non-provisional Application No. 10/374,780, filed February 25, 2003, which claims priority from U.S. Non-provisional Application No. 09/934,455, filed August 22, 2001, which in turn claims priority from U.S. Provisional Application No. 60/227,439, filed August 22, 2000~~; and, this application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Patent Application No. 10/225,068, filed August 9, 2002 (pending)~~, which claims priority from U.S. Provisional Application No.60/336,049, filed November 19, 2001 and U.S. Provisional Patent Application No. 60/310,847, filed August 9, 2001~~; and, this application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Patent Application No. 10/225,066, filed August 9, 2002 (pending) which is a continuation-in-part of prior U.S. Patent Application No. 10/171,468, filed June 14, 2002 (now abandoned); ~~and U.S. Non-provisional Application No. 10/225,067, filed August 9, 2002; the~~ and, this application is a continuation-in-part of prior U.S. Patent Application No. 09/934,455, filed August 22, 2001 (now abandoned). The entire contents of ~~which~~ each of these applications are ~~hereby~~ incorporated herein by reference.

Please add the following new paragraph to the specification on page 1, line 22, after the first paragraph of priority claims and before "Field of the Invention".

The claimed invention, in the field of functional genomics and the characterization of plant genes for the improvement of plants, was made by or on behalf of Mendel Biotechnology, Inc. and Monsanto Corporation as a result of activities undertaken within the scope of a joint research agreement, said agreement having been in effect on or before the date the claimed invention was made.

Please replace the paragraph on page 9, lines 21-24, with the following amended paragraph:

CD-ROM1 is a read-only memory computer-readable compact disc and contains a copy of the Sequence Listing in ASCII text format. The Sequence Listing is named "MBI0049CIP.ST25.txt". This file was created on October 9, 2003, and is 139 kilobytes in size. The copies of the Sequence Listing on the CD-ROM disc are hereby incorporated by reference in their entirety.

Please replace the paragraph on page 16, line 26 through page 17, line 3, with the following amended paragraph:

With regard to polynucleotide variants, differences between presently disclosed polynucleotides and polynucleotide variants are limited so that the nucleotide sequences of the former and the latter are closely similar overall and, in many regions, identical. Due to the degeneracy of the genetic code, differences between the former and latter nucleotide sequences [[o]] may be silent (i.e., the amino acids encoded by the polynucleotide are the same, and the variant polynucleotide sequence encodes the same amino acid sequence as the presently disclosed polynucleotide. Variant nucleotide sequences may encode different amino acid sequences, in which case such nucleotide differences will result in amino acid substitutions, additions, deletions, insertions, truncations or fusions with respect to the similar disclosed polynucleotide sequences. These variations result in polynucleotide variants encoding polypeptides that share at least one functional characteristic. The degeneracy of the genetic code also dictates that many different variant polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

Please replace the paragraph on page 17, lines 19-25, with the following amended paragraph:

"Splice variant" or "polynucleotide splice variant" as used herein refers to alternative forms of RNA transcribed from a gene. Splice variation naturally occurs as a result of alternative sites being spliced within a single transcribed RNA molecule or between separately transcribed RNA molecules, and may result in several different forms of mRNA transcribed from the same gene. ~~This~~ Thus, splice variants may encode polypeptides having different amino acid sequences, which may or may not have similar functions in the organism. "Splice variant" or "polypeptide splice variant" may also refer to a polypeptide encoded by a splice variant of a transcribed mRNA.

Please replace the paragraph on page 68, line 19 through page 69, line 6, with the following amended paragraph:

Suppression of endogenous transcription factor gene expression can also be achieved using RNA interference, or RNAi. RNAi is a post-transcriptional, targeted gene-silencing technique that uses double-stranded RNA (dsRNA) to incite degradation of messenger RNA (mRNA) containing the same sequence as the dsRNA (Constans, (2002) The Scientist 16:36). Small interfering RNAs, or siRNAs are produced in at least two steps: an endogenous ribonuclease cleaves longer dsRNA into shorter, 21-23 nucleotide-long RNAs. The siRNA segments then mediate the degradation of the target mRNA (Zamore, (2001) Nature Struct. Biol., 8:746-50). RNAi has been used for gene function determination in a manner similar to antisense oligonucleotides (Constans, (2002) The Scientist 16:36). Expression vectors that continually express siRNAs in transiently and stably transfected cells have been engineered to express small hairpin RNAs (shRNAs), which get processed in vivo into siRNAs-like molecules capable of carrying out gene-specific silencing (Brummelkamp et al., (2002) Science 296:550-553, and Paddison, et al. (2002) Genes & Dev. 16:948-958). Post-transcriptional gene silencing by double-stranded RNA is discussed in further detail by Hammond et al. (2001) Nature Rev Gen 2: 110-119, Fire et al. (1998) Nature 391: 806-811 and Timmons and Fire (1998) Nature 395: 854. Vectors in which RNA encoded by a transcription factor or transcription factor homolog cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in US Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Please replace the paragraph on page 69, lines 7-19, with the following amended paragraph:

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in US Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double~~-strand~~ stranded RNA (Sharp (1999) Genes and Development 13: 139-141). Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of Agrobacterium tumefaciens. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homolog gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation. Such methods are well known to those of skill in the art (See for example Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific Publishing Co. Pte. Ltd., River Edge, NJ).

Please replace the paragraph on page 97, lines 21-24, with the following amended paragraph:

Similarly, the amino acid sequences of the three CBF polypeptides range from 84 to 86% identity. An alignment of the three amino ~~acidic~~ acid sequences reveals that most of the differences in amino acid sequence occur in the acidic C-terminal half of the polypeptide. This region of CBF1 serves as an activation domain in both yeast and Arabidopsis (not shown).

Please replace the paragraph on page 106, lines 2-7, following "Abstract of the Disclosure", with the following amended paragraph:

The invention relates to ~~plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce~~ transgenic plants transformed with nucleic acids that encode plant transcription factors that regulate tolerance to abiotic stresses. These transgenic plants have ~~having advantageous properties, including~~ improved drought and other ~~osmotic~~ abiotic stress tolerance, as compared to wild-type or ~~reference~~ control plants. ~~Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods to identify related sequences and is also disclosed.~~